WHAT IS CLAIMED IS:

1. A method for high-throughput nucleotide polymorphism analysis of a nucleic acid sample from a subject comprising:

(a) contacting a plurality of peptide-labeled oligonucleotide probes with the nucleic acid sample in solution, under conditions conducive to hybridization of the probes to nucleic acid in the sample; and

(b) detecting one or more probes of the plurality that hybridize to nucleic acid in the sample using an antibody array comprising antibodies immunospecific to one or more of the peptide labels.

2. The method of claim 1, wherein detecting the one or more probes is carried out without using PCR or MutS.

3. A method for screening a nucleic acid sample from one or more subjects for the presence of a polymorphism comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first marker covalently attached to a first detectable label, and a second marker covalently attached to a second detectable label that produces a signal distinguishable from the first detectable label; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(f) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(g) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein a difference between the first ratio and the second ratio indicates that a polymorphism is identified.

4. A method for screening a nucleic acid sample from one or more subjects for the presence of a polymorphism comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more nucleotide polymorphism-specific oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with (i) a first partner molecule with the ability to specifically bind the first marker, and (ii) a second partner molecule with the ability to specifically bind the second marker, said first partner molecule comprising a first detectable label and said second partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(f) removing material not bound to the solid phase surface;

(g) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(h) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(i) detecting or measuring from the solid phase surface a third signal from the detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein a difference between the first ratio and the second ratio indicates that a polymorphism is identified.

5. A method for screening a nucleic acid sample from one or more subjects for the presence of a polymorphism comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more nucleotide polymorphism-specific oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with a first primary partner molecule, with the ability to bind the first marker, and a second primary partner molecule with the ability to bind the second marker;

(f) removing material not bound to the solid phase surface;

(g) contacting the solid phase surface with (i) a first secondary partner molecule, with the ability to bind the first primary partner molecule, said first secondary partner molecule comprising a first detectable label, and (ii) a second secondary partner molecule, with the ability to bind the second primary partner molecule, said second secondary partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(h) removing material not bound to the solid phase surface;

(i) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(j) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(k) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein a difference between the first ratio and the second ratio indicates that a polymorphism is identified.

6. A composition comprising one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes bound to one or more antibodies of an antibody array.

7. The method of claim 3, 4, or 5, wherein at least one of the one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes comprises:
(a) a peptide covalently attached to the 5' end of the oligonucleotide;
(b) a first marker at the penultimate 5' position of the oligonucleotide; and
(c) a second marker at the 3'-end of the oligonucleotide.

8. The method of claim 3, 4, or 5, wherein the solid phase surface comprises a plurality of loci, wherein each locus is capable of specifically binding to one of the one or more oligonucleotide probes via the peptide of the peptide-labeled oligonucleotide and wherein the peptide is covalently attached to the 5' end of the oligonucleotide.

9. The method of claim 4 wherein the first or second marker is covalently attached to a biotin moiety and the first or second partner molecule is avidin or streptavidin.

10. The method of claim 5 wherein the first or second marker is covalently attached to a biotin moiety and the first or second primary partner molecule is avidin or streptavidin.

11. The method of claim 4 wherein the first or second marker is covalently attached to a carbohydrate moiety and the first or second partner molecule is a lectin.

12. The method of claim 5 wherein the first or second marker is covalently linked to a carbohydrate moiety and the first or second primary partner molecule is a lectin.

13. The method of claim 4 wherein the first partner molecule is an antibody that binds specifically to the first marker and the second partner molecule is an antibody that binds specifically to the second marker.

14. The method of claim 5 wherein the first and second primary partner molecules are distinct primary antibodies, and the first and second secondary partner molecules are distinct secondary antibodies.

15. The method of claim 3, 4, or 5 wherein either or both the first detectable label or the second detectable label is an enzyme, a fluorophore, a chemiluminescent label, or a radioisotope.

16. The method of claim 3, 4, or 5 wherein either or both the first detectable marker or the second detectable marker is a fluorophore.

17. A method for identifying a polymorphism in a nucleic acid sample from one or more subjects comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first marker covalently attached to a first detectable label, and a second marker covalently attached to a second detectable label that produces a signal distinguishable from the first detectable label; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes ;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(f) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(g) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein the first ratio at least 35% greater than the second ratio indicates that a polymorphism is identified.

18. A method for identifying a polymorphism in a nucleic acid sample from one or more subjects comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more nucleotide polymorphism-specific oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with (i) a first partner molecule with the ability to specifically bind the first marker, and (ii) a second partner molecule with the ability to specifically bind the second marker, said first partner molecule comprising a first detectable label and said second partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(f) removing material not bound to the solid phase surface;

(g) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(h) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(i) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio, wherein the first ratio at least 35% greater than the second ratio indicates that a polymorphism is identified.

19. A method for identifying a polymorphism in a nucleic acid sample from one or more subjects comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more nucleotide polymorphism-specific peptide-labeled oligonucleotide probes, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more nucleotide polymorphism-specific oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with a first primary partner molecule, with the ability to bind the first marker, and a second primary partner molecule with the ability to bind the second marker;

(f) removing material not bound to the solid phase surface;

(g) contacting the solid phase surface with (i) a first secondary partner molecule, with the ability to bind the first primary partner molecule, said first secondary partner molecule comprising a first detectable label, and (ii) a second secondary partner molecule, with the ability to bind the second primary partner molecule, said second secondary partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(h) removing material not bound to the solid phase surface;

(i) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(j) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(k) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio, wherein the first ratio at least 35% greater than the second ratio indicates that a polymorphism is identified.

20. The method of claim 3, 4, 5, 17, 18, or 19, wherein the solid phase surface comprises a plurality of loci, wherein each locus comprises an antibody specific to one or more of the peptides of the peptide-labeled oligonucleotide probes.

21. The method of claim 3, 4, 5, 17, 18, or 19, wherein the solid phase surface is a plastic chip.

22. The method of claim 3, 4, 5, 17, 18, or 19, wherein the solid phase surface is the well of a microtiter plate.

23. The method of claim 1, 3, 4, 5, 17, 18, or 19, wherein the nucleic acid in the sample is less than 2 μg.

24. The method of claim 1, 3, 4, 5, 17, 18, or 19, wherein the nucleic acid in the sample is selected from the group consisting of genomic DNA and cDNA.

25. The method of claim 1, 3, 4, 5, 17, 18, or 19, wherein the nucleic acid in the sample is genomic DNA .

26. The method of claim 1, 3, 4, 5, 17, 18, or 19, wherein the nucleic acid in the sample is cDNA.

27. The method of claim 1, 3, 4, 5, 17, 18, or 19, wherein the nucleic acid in the sample is double stranded DNA.

28. The method of claim 1, 3, 4, 5, 17, 18, or 19, wherein the nucleic acid in the sample is single stranded DNA.

29. The method of claim 3, 4, 5, 17, 18, or 19, wherein cleaving the hybrid molecules at mismatched base pairs is carried out by contacting said hybrid molecules with one or more specific nucleases under conditions that allow cleavage of said hybrid molecules at mismatched base pairs.

30. The method of claim 3, 4, 5, 17, 18, or 19, wherein cleaving the hybrid molecules at mismatched base pairs is carried out by contacting said hybrid molecules with *E. coli* endonuclease V and S1 nuclease under conditions that allow cleavage of said hybrid molecules at mismatched base pairs.

31. The method of claim 3, 4, 5, 17, 18, or 19, wherein the first and second detectable labels are fluorophores that absorb at the same wavelength but emit at a distinct frequency.

32. A method for detecting or measuring the presence of an alternatively spliced RNA transcript in a sample from a subject comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more peptide-labeled oligonucleotide probes, comprising the sequence of a known splice-site junction, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first marker covalently attached to a first detectable label, and a second marker covalently attached to a second detectable label that produces a signal distinguishable from the first detectable label; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(f) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(g) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein a difference between the first ratio and the second ratio indicates that an alternatively spliced RNA transcript is in the sample.

33. A method for detecting or measuring the presence of an alternatively spliced RNA transcript in a sample from a subject comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more peptide-labeled oligonucleotide probes, comprising the sequence of a known splice-site junction, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with (i) a first partner molecule with the ability to specifically bind the first marker, and (ii) a second partner molecule with the ability to specifically bind the second marker, said first partner molecule comprising a first detectable label and said second partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(f) removing material not bound to the solid phase surface;

(g) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(h) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(i) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein a difference between the first ratio and the second ratio indicates that an alternatively spliced RNA transcript is in the sample.

34. A method for detecting or measuring the presence of an alternatively spliced RNA transcript in a sample from a subject comprising:

(a) contacting the nucleic acid sample in solution with one or more peptide-labeled oligonucleotide probes comprising the sequence of a known splice-site junction sequence, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with a first primary partner molecule, with the ability to bind the first marker, and a second primary partner molecule with the ability to bind the second marker;

(f) removing material not bound to the solid phase surface;

(g) contacting the solid phase surface with a first secondary partner molecule, with the ability to bind the first primary partner molecule, said first secondary partner molecule comprising a first detectable label, and a second secondary partner molecule, with the ability to bind the second primary partner molecule, said second secondary partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(h) removing material not bound to the solid phase surface;

(i) detecting or measuring a first signal from the first detectable label and a second signal from the second detectable label;

(j) cleaving the hybrid molecules at mismatched base pairs; and

(k) detecting or measuring a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the

second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein a difference between the first ratio and the second ratio indicates that an alternatively spliced RNA transcript is in the sample.

35. A method for detecting or measuring the presence of an alternatively spliced RNA transcript in a sample from a subject comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more peptide-labeled oligonucleotide probes comprising the sequence of a known splice-site junction sequence, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first marker covalently attached to a first detectable label, and a second marker covalently attached to a second detectable label that produces a signal distinguishable from the first detectable label; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) detecting or measuring a first signal from the first detectable label and a second signal from the second detectable label;

(f) cleaving the hybrid molecules at mismatched base pairs; and

(g) detecting or measuring a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein the first ratio at least 35% greater than the second ratio indicates that an alternatively spliced RNA transcript is in the sample.

36. A method for detecting or measuring the presence of an alternatively spliced RNA transcript in a sample from a subject comprising the following steps in the order stated:

(a) contacting the nucleic acid sample in solution with one or more peptide-labeled oligonucleotide probes comprising the sequence of a known splice-site junction sequence, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a

second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the first marker with a first partner molecule and the second marker with a second partner molecule, said first partner molecule comprising a first detectable label and said second partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(f) removing material not bound to the solid phase surface;

(g) detecting or measuring a first signal from the first detectable label and a second signal from the second detectable label;

(h) cleaving the hybrid molecules at mismatched base pairs; and

(i) detecting or measuring a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein the first ratio at least 35% greater than the second ratio indicates that an alternatively spliced RNA is in the sample.

37. A method for detecting or measuring the presence of an alternatively spliced RNA transcript in a sample from a subject comprising:

(a) contacting the nucleic acid sample in solution with one or more peptide-labeled oligonucleotide probes comprising the sequence of a known splice-site junction sequence, under conditions conducive to hybridization of the probes to nucleic acid in the sample; each probe comprising a first and a second marker; such that one or more hybrid molecules are formed between the nucleic acid and one or more oligonucleotide probes;

(b) capturing at least one of the one or more hybrid molecules on a solid phase surface;

(c) contacting the solid phase surface with mung bean nuclease, under conditions wherein the nuclease is active;

(d) removing material not bound to the solid phase surface;

(e) contacting the solid phase surface with a first primary partner molecule, with the ability to bind the first marker, and a second primary partner molecule with the ability to bind the second marker;

(f) removing material not bound to the solid phase surface;

(g) contacting the solid phase surface with (i) a first secondary partner molecule, with the ability to bind the first primary partner molecule, said first secondary partner molecule comprising a first detectable label, and (ii) a second secondary partner molecule, with the ability to bind the second primary partner molecule, said second secondary partner molecule comprising a second detectable label that produces a signal distinguishable from the first detectable label;

(h) removing material not bound to the solid phase surface;

(i) detecting or measuring from the solid phase surface a first signal from the first detectable label and a second signal from the second detectable label;

(j) cleaving the hybrid molecules on the solid phase surface at mismatched base pairs; and

(k) detecting or measuring from the solid phase surface a third signal from the first detectable label and a fourth signal from the second detectable label, determining a first ratio of the second signal to the first signal, and a second ratio of the fourth signal to the third signal, and comparing the first ratio to the second ratio,

wherein the first ratio at least 35% greater than the second ratio indicates that an alternatively spliced RNA transcript is in the sample.

38. The method of claim 1, 3, or 4 wherein the subject is a plant.

39. The method of claim 1, 3, or 4 wherein the subject is a virus, a bacterium, a yeast, or a fungus.

40. The method of claim 1, 3, or 4 wherein the subject is a mammal.

41. The method of claim 1, 3, or 4 wherein the subject is equine, porcine, ovine, bovine, canine, feline, or human.

42. The method of claim 1, 3, or 4 wherein the subject is a human.

43. The method of claim 1, 3, or 4 wherein the subject is a plurality of human subjects that exhibit a phenotype of interest.

44. A two-molecule peptide-labeled oligonucleotide probe comprising a first molecule comprising a first sequence of nucleotides, which molecule is covalently attached to a peptide label; and a second molecule comprising a second sequence of nucleotides complementary to the first sequence and contiguous with additional nucleotides complementary to a wild-type or variant form of a nucleotide polymorphism of interest and its flanking regions.

45. A two-molecule peptide-labeled oligonucleotide probe comprising a first molecule, the nucleotide sequence of which consists of a first sequence of from 15 to 25 nucleotides, which molecule is covalently attached to a peptide label; and a second molecule, the nucleotide sequence of which consists of a second sequence of from 15 to 25 nucleotides complementary to the first sequence and contiguous with from 30 to 40 nucleotides complementary to a wild-type or variant form of a nucleotide polymorphism of interest and its flanking regions.

46. The probe of claim 44 or 45, wherein the second molecule comprises at least one detectable marker.

47. The probe of claim 46, wherein at least one detectable marker is a fluorophore.

48. The probe of claim 44 or 45, wherein at least one nuclease-resistant nucleotide base derivative occurs at a position within three nucleotides from the transition from double-stranded to single-stranded structure when the first molecule is hybridized to the second molecule.

49. The probe of claim 44 or 45, wherein six nuclease-resistant nucleotide base derivatives occur at positions within three nucleotides from the transition from double-stranded to single-stranded structure when the first molecule is hybridized to the second molecule.

50. A kit comprising in one or more containers a purified first molecule comprising a first sequence of nucleotides, which molecule is covalently attached to a peptide label, and a purified second molecule comprising a second sequence of nucleotides complementary to the first sequence and contiguous with additional nucleotides complementary to a wild-type or variant form of a nucleotide polymorphism of interest and its flanking regions.